

Alignment Report of Untitled, using Clustal method with PAM250 residue weight table.

FIGURE 1A

Alignment Report of Untitled, using Clustal method with PAM250 residue weight table.

FIGURE 1B

Alignment Report of Unfiled, using Clustal method with PAM250 residue weight table.

	330	340	350	360
238 S E S S E E V D C D G C T T D W K K G K N V T V K T I K K Q K H K G R G T V				Q99733 in SwissProt-1.pro
238 S E S S E E V D C D G C T T D W K K G K N V T V K T I K K Q K H K G R G T V				3319977 in GenPept-1.pro
319 P Y R G T A Y S T G C E D D N N G K N V T L K P I K K Q K H R I W G T I				5931610 in GenPept-1.pro
179 - - - - -				hNARC10C orf1-1.pro
319 P Y R G T A Y S T G C D E D W N E G K N V T L R T I K K Q R H R V W G T V				P51860 in SwissProt-1.pro
191 - - D E T I L K T K A T G T E W Y P G K C L T Q K V L K K P K - K ' G S K N A				1161252 in GenPept-1.pro
	370	380	390	400
278 K Q V D P V E S E F E N P L K A S G D I G E S L D E D S E F T L A S - -				Q99733 in SwissProt-1.pro
278 K Q V D P V E S E F E N P L K A S G D I G E S L D E D S E F T L A S - -				3319977 in GenPept-1.pro
359 R V E D F B K D S E F E N P L K A S G D I G E S L D E D S E F T L A S - -				5931610 in GenPept-1.pro
179 - - - - -				hNARC10C orf1-1.pro
359 R V E D F E K D S E F E N P L K A S G D I G E S L D E D S E F T L A S - -				P51860 in SwissProt-1.pro
228 K P T T E S C E S E F E N P L K A P E V P E D D A D I D E D L A E E L Q N Q M				1161252 in GenPept-1.pro
	410	420	430	440
316 - - R E F E F F E D V P R A V E Y E T G E A I E D D N - - F E E G E E				Q99733 in SwissProt-1.pro
316 - - R E F E F F E D V P R A V E Y E T G E A I E D D N - - F E E G E E				3319977 in GenPept-1.pro
390 - - R L C H N T R Y T I P R S V I E F S I G D A E S Q Q E G V V R E V N D				5931610 in GenPept-1.pro
179 - - - - -				hNARC10C orf1-1.pro
390 - - R L C H N T Y T I P R S V I E F S G D A E S Q Q E G V V R E V N D				P51860 in SwissProt-1.pro
268 E Q F Y D E S T T D K R I S P H A V S W E T G E A A Q G D E F E D L E D D E D				1161252 in GenPept-1.pro
	450	460	470	480
352 G E E F E F G D E - - E G E D E D D A - - E I N P K V				Q99733 in SwissProt-1.pro
352 G E E F E F G D E - - E G E D E D D A - - D V N P K V				3319977 in GenPept-1.pro
427 A I Y D K I I Y D W M A A I E E V K A C C K N L E A L V E D I D R				5931610 in GenPept-1.pro
179 - - - - -				hNARC10C orf1-1.pro
427 E I Y S K I I Y D W M A A I E E V K A C C K N L E A L V E D I D R				P51860 in SwissProt-1.pro
308 E G D E D D E D D E E D D E E D D E E D D T K T K K S G K A Q A G D G				1161252 in GenPept-1.pro

FIGURE 1C

Alignment Report of Untitled, using Clustal method with PAM250 residue weight table.

375
375
460
182
460
348 D G E R P P E C K Q Q

490

Q99733 in SwissProt-1.pro
3319977 in GenPept-1.pro
5931610 in GenPept-1.pro
hNARC10C orf1-1.pro
P51860 in SwissProt-1.pro
1161252 in GenPept-1.pro

FIGURE 1D

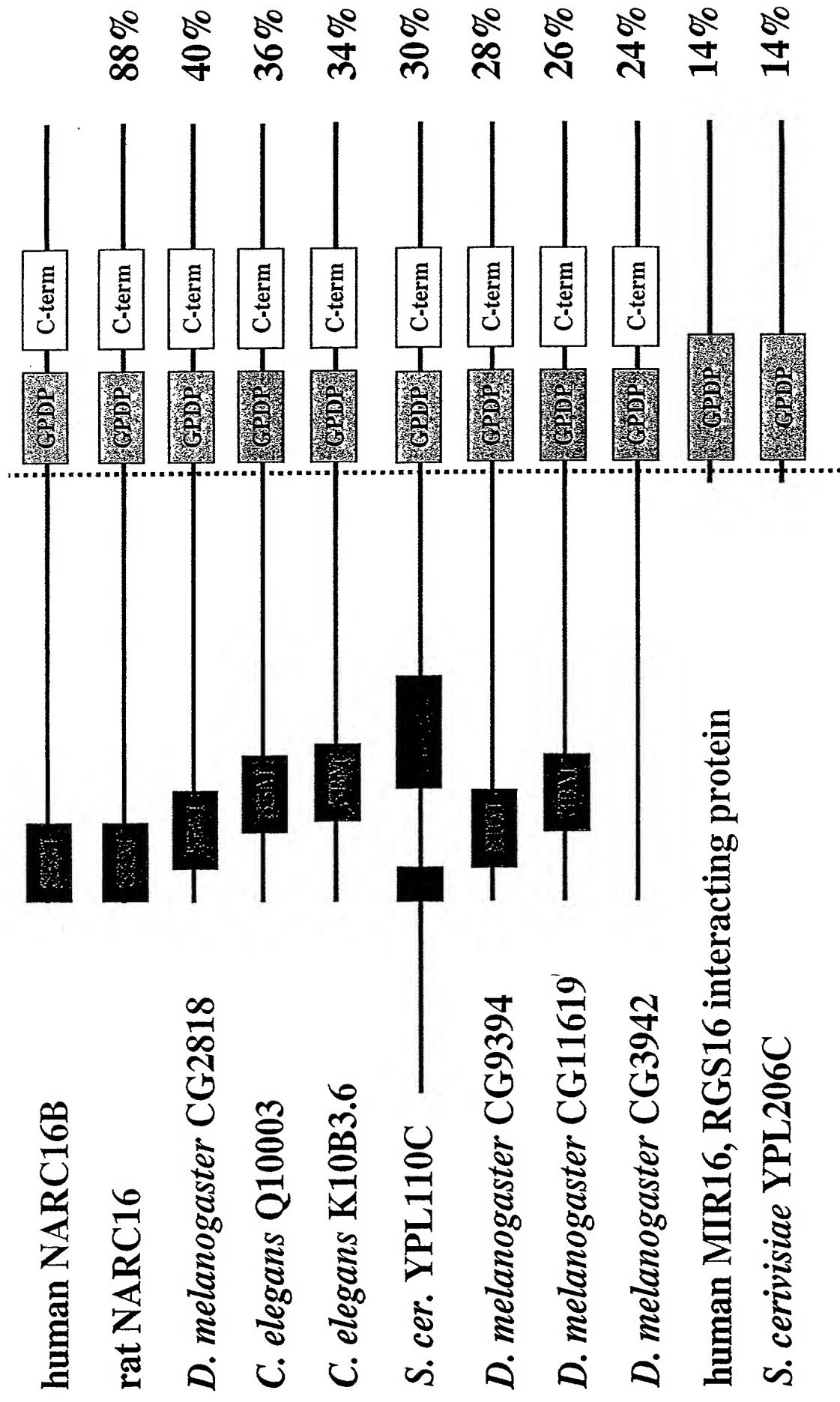


FIGURE 2

Alignment Report of truncatedNARC16GDPclustal.MEG, using Clustal method with PAM250 residue weight table.

Sequence logo for the PENTIASE region showing conservation across 133 homologs. The y-axis represents sequence position from 1 to 133. The x-axis shows amino acids: H, R, G, A, D, V, E, L, K, N, S, M, T, I, V, M, G, S, S, A, M, A, D, S, N, E, K, I, V, I, A, H, R, G, A, S, G, - (stop). The logo is color-coded: black for H, red for R, blue for G, green for A, orange for D, yellow for V, purple for E, grey for L, brown for K, pink for N, light blue for S, light green for M, light orange for T, light pink for I, light blue for V, light green for M, light orange for G, light pink for S, light blue for S, light green for A, light orange for M, light pink for A, light blue for D, light green for S, light orange for N, light pink for E, light blue for K, light green for I, light orange for V, light pink for I, light blue for A, light green for H, light orange for R, light pink for G, light blue for A, light green for S, light orange for G, light pink for - (stop). A legend on the right indicates: black box = + Majority, grey box = - Majority, black text = human match.

FIGURE 3A

Alignment Report of truncatedNARC16GDPclustal.MEG, using Clustal method with PAM250 residue weight table.

FIGURE 3B

Alignment Report of truncatedNARC16GDPclustal.MEG, using Clustal method with PAM250 residue weight table.

卷之三

FIGURE 3C

Alignment Report of truncatedNARC16GPDPclustal.MEG, using Clustal method with PAM250 residue weight table.

GI - L X H L I L E K A		+ Majority		human match	
310	320	330	340	350	
547 N	- K I T R E N R L	- - - M I G S I N K N G L	- - - N I F A W	- - - A A	yhdW.seq
832 C P D Y H M E E B T S Q P G N I K L T G M V Q D A Q Q N K L	- - - R V M Q L K D A G L	- - - V H P Y R S D K L	- - - P E b2239.seq		
559 S R H E N H K L U N K A	- - - R V I T V Y T N K R Q R	- - - R I I V Y T N K R Q R	- - - A A b3449.seq		
586 P V I T - - - P A	- - - R V R G F H A A G R	- - - Q V H A W D E P D V	- - - M H Rv0317c.seq		
619 C P S S P A K E Y P Q	- - - L V D R S A A Q G R	- - - A V Y C W N D E Y E D	- - - I D Rv3842c.seq		
565 L H - P . T N M Y E K F	- - - P D M V L S	- - - L Q L P L - G L	- - - L N A05 orf241a.seq		
847 K A K G L V I F C W G D D T N D P E N R R K L K E L G V N G L I Y D R I Y D W M P E Q R N I F Q V E hNARC16 CtermG.seq					
360	370	380	390	400	
X L L D V G V D		+ Majority		human match	
969 K L Q A M G A D	- - - G I V D Y P D F I	- - - K D G K H	- - - E I	yhdW.seq	
967 Y T P A V N Q L	- - - Y D A L Y N K A G V N G L F	- - - T D F P D K A V K F L N K E	- - - b2239.seq		
667 E L E R W E D D	- - - C I C T D A I D V I	- - - G P N F	- - - A Q	b3449.seq	
676 T L T D M D V D	- - - G I I T D R A D L L R D - V	- - - L I A R G E W	- - - D G	Rv0317c.seq	
727 F C R E E G A	- - - W I G T H H D G R T K A W L	- - - E D G P R A N G	- - - T R	Rv3842c.seq	
649 S E V K F H Q F	- - - R Q D R M Y A Q T A	- - - N K K F E V	- - - A 05 orf241a.seq		
997 O L E R L K O E L P E L K S C L C P T V S R F V P S S E C G E S D I H V D A N G I D N V E N A					

FIGURE 3D

Alignment Report of truncatedNARC16GPDpClustal.MEG, using Clustal method with PAM250 residue weight table.

	human match
+	Majority
-	Majority
—	—
730	yhdW.seq
1075	b2239.seq
742	b3449.seq
769	Rv0317c.seq
823	Rv3842c.seq
724	A05 or f241a.seq
1138	hNARC16_CtermLG.seq

FIGURE 3E

Input file flhbNARC10C; Output File flhbNARC10C.pat
Sequence length 2034

GTCGACCCACGCGTCCGGCAAGATCTCTCTGGACCAGCTCGGGTGCAGGGCCTCTGCGGGAGCCCTCCTAGACCTCTGC 79
 M A D S E N Q G P A E P S Q A A 16
 GGCTTCTCCTCTAAC ATG GCC GAC TCG GAA AAC CAG GGG CCT GCG GAG CCT AGC CAG GCG GCG 142
 A A A E A A A E E V M A E G G A Q G G D 36
 GCA GCG GCG GAG GCA GCG GCA GAG GAG GTA ATG GCG GAA GGC GGT GCG CAG GGT GGA GAC 202
 C D S A A G D P D S A A G Q M A E E P Q 56
 TGT GAC AGC GCG GCT GGT GAC CCT GAC AGC GCG GCT GGT CAG ATG GCT GAG GAG CCC CAG 262
 T P A E N A P K P K N D F I E S L P N S 76
 ACC CCT GCA GAG AAT GCC CCA AAG CCG AAA AAT GAC TTT ATC GAG AGC CTG CCT AAT TCG 322
 V K C R V L A L K K L Q K R C D K I E A 96
 GTG AAA TGC CGA GTC CTG GCC CTC AAA AAG CTG CAG AAG CGA TGC GAT AAG ATA GAA GCC 382
 K F D K E F Q A L E K K Y N D I Y K P L 116
 AAA TTT GAT AAG GAA TTT CAG GCT CTG GAA AAA AAG TAT AAT GAC ATC TAT AAG CCC CTA 442
 L A K I Q E L T G E M E G C A W T L E G 136
 CTC GCC AAG ATC CAA GAG CTC ACC GGC GAG ATG GAG GGG TGT GCA TGG ACC TTG GAG GGG 502
 E E E E E Y E D D E E G E D E E E 156
 GAG GAG GAG GAG GAA GAG TAC GAG GAT GAC GAG GAG GGG GAA GAC GAG GAG GAG 562
 E E A A E A A A G A K H D D A H A E M 176
 GAG GAG GCT GCG GCA GAG GCT GCC GCG GGG GCC AAA CAT GAC GAT GCG CAC GCG GAG ATG 622
 P D D A K K * 183
 CCT GAT GAC GCC AAG AAG TAA 643
 GGGGGCAGAGATGGATGAAAGAGAAAGCCCACGAAGAAAAAGCCTGGTTTGTGTTTCCAGAAATATCGATGGACTTA 722
 AAAAGGCTCAGGTTTTGACCAAAATACAATGTGAATTATCTGACATTCTAAATAGATTAATAAAGCAATTAG 801
 ATCCTGGCCAGCTCGATTCAAATTGACTTTGACATTGAAACATAATAATATCAAAGGTGTTAAAGAAAATCTGAAT 880
 TAAACCCAAAATTATGTTTCAATGGCTCTCTGAGGATTGAGGTTTACAAAGGGTGTAGCAGATGCGAAGTAAAG 959
 AACGTCACTTGAAACCCATTCACTCACACAGCATCGTACACATGGAACACCCAAGCCATGACTGAACACGTTCTCAG 1038
 TGCTTAATTCTTAAATTCTTACTCATGACATTGCGAGTGCAGAGAAGGAGAACCCAGAAAACGTCATCTTGA 1117
 GACTTTGCTTTGTAACGCGACATCAGCTTACACTTCACAGGAGATTGATGGCATTGAGGAAGATTGCAATGGAGAT 1196
 CATGACACTACTGTTAATAAGGCCAGGAAACTGCCATTCAAGTTCTGAAAAATGTTTGAGTATTGAAATTAGAGA 1275
 AACAAACATGGTTCCAAGAAGGAGGGTGTAAAACCTGAAATACTGTCACATATGTTAGTTACAATCTCATG 1354
 TTTGTTGTTCTTACTGACTGCTATTACAAACACGTTAAACACGTTAAACACGTTAAACACGTTAAATCACTTAC 1433
 TAGCGTTTAGAAATATTAATTACTGTAAGAGATGTAGAAATGTAGCAAATTATGTAAGCATGTTGATCCAGCGTTAT 1512
 GTACTTTGCGCTTGTGACGTCTTCTGTCATGTTAGCTGTGCCCCCTACCCAGCTCAGAAGTAGAAAGG 1591
 AGCTTAATGTTGGAAAAATATATACTTGAAAGAACCAATCCAAGTGTGCCCCCTACCCAGCTCAGAAGTAGAAAGG 1670
 GTTTAAGTTGCTTGTATTAGCTGTGCCCCATTATTGCTATGTTAGCTGTGAAATCTGACATATTAAATTATAAAATGGTGCATA 1749
 ATCAAATTTACTGCTTGAGGACAGATGCATACAGTAAGGATTGAGGAAGAATATTTAATGTAAGACTCTTAGC 1828
 TTCTGTTGGGTTTGAATTATGTTGAGGACAGATGCATACAGTAAGGATTGAGGAAGAATATTTAATGTAAGACTCTTAGC 1907
 TTAATAAAACAGTATTTCAAAAAATAAAAAAGGGCGGCCGC 1986
 AAAAAAAAAAAAAAAAAAAGGGCGGCCGC 2034

Input file fthuNARC16B; Output File fthuNARC16B.pat
Sequence length 3206

GTCGACCCACGCGTCCGGCGAGGCACGGACGGCGGGCGCCGGTACCTCTGCCCGCGTCTCGCTCTCGGGCGGGGC 79
 M T P 3
 GGCGGGCGACGCGGACCTGCGGACTAGCGAACCCGGAGCACGACATCATAAAATCCATCAGA ATG ACA CCT 153
 S Q V A F E I R G T L L P G E V F A I C 23
 TCT CAG GTT GCC TTT GAA ATA AGA GGA ACT CTT TTA CCA GGA GAA GTT TTT GCG ATA TGT 213

FIGURE 4A

G	S	C	D	A	L	G	N	W	N	P	Q	N	A	V	A	L	L	P	E	43
GGA	AGC	TGT	GAT	GCT	TTG	GGA	AAC	TGG	AAT	CCT	CAA	AAT	GCT	GTG	GCT	CTT	CTT	CCA	GAG	273
N	D	T	G	E	S	M	L	W	K	A	T	I	V	L	S	R	G	V	S	63
AAT	GAC	ACA	GGT	GAA	AGC	ATG	CTA	TGG	AAA	GCA	ACC	ATT	GTA	CTC	AGT	AGA	GGA	GTA	TCA	333
V	Q	Y	R	Y	F	K	G	Y	F	L	E	P	K	T	I	G	G	P	C	83
GTT	CAG	TAT	CGC	TAC	TTC	AAA	GGG	TAC	TTT	TTA	GAA	CCA	AAG	ACT	ATC	GGT	GGT	CCA	TGT	393
Q	V	I	V	H	K	W	E	T	H	L	Q	P	R	S	I	T	P	L	E	103
CAA	GTG	ATA	GTT	CAC	AAG	TGG	GAG	ACT	CAT	CTA	CAA	CCA	CGA	TCA	ATA	ACC	CCT	TTA	GAA	453
S	E	I	I	I	D	D	G	Q	F	G	I	H	N	G	V	E	T	L	D	123
AGC	GAA	ATT	ATT	ATT	GAC	GAT	GGA	CAA	TTT	GGA	ATC	CAC	AAT	GGT	GTT	GAA	ACT	CTG	GAT	513
S	G	W	L	T	C	Q	T	E	I	R	L	R	L	H	Y	S	E	K	P	143
TCT	GGA	TGG	CTG	ACA	TGT	CAG	ACT	GAA	ATA	AGA	TTA	CGT	TTG	CAT	TAT	TCT	GAA	AAA	CCT	573
P	V	S	I	T	K	K	K	L	K	K	S	R	F	R	V	K	L	T	L	163
CCT	GTG	TCA	ATA	ACC	AAG	AAA	AAA	TTA	AAA	AAA	TCT	AGA	TTT	AGG	GTG	AAG	CTG	ACA	CTA	633
E	G	L	E	E	D	D	D	R	V	S	P	T	V	L	H	K	M	S	183	
GAA	GCC	CTG	GAG	GAA	GAT	GAC	GAT	GAT	AGG	GTA	TCT	CCC	ACT	GTA	CTC	CAC	AAA	ATG	TCC	693
N	S	L	E	I	S	L	I	S	D	N	E	F	K	C	R	H	S	Q	P	203
AAT	AGC	TTG	GAG	ATA	TCC	TTA	ATA	AGC	GAC	AAT	GAG	TTC	AAG	TGC	AGG	CAT	TCA	CAG	CCG	753
E	C	G	Y	G	L	Q	P	D	R	W	T	E	Y	S	I	Q	T	M	E	223
GAG	TGT	GGT	TAT	GGC	TTG	CAG	CCT	GAT	CGT	TGG	ACA	GAG	TAC	AGC	ATA	CAG	ACG	ATG	GAA	813
P	D	N	L	E	L	I	F	D	F	F	E	E	D	L	S	E	H	V	V	243
CCA	GAT	AAC	CTG	GAA	CTA	ATC	TTT	GAT	TTT	TTC	GAA	GAA	GAT	CTC	AGT	GAG	CAC	GTA	GTT	873
Q	G	D	A	L	P	G	H	V	G	T	A	C	L	L	S	S	T	I	A	263
CAG	GGT	GAT	GCC	CTT	GGA	CAT	GTG	GGT	ACA	GCT	TGT	CTC	TTA	TCA	TCC	ACC	ATT	GCT	933	
E	S	G	K	S	A	G	I	L	T	L	P	I	M	S	R	N	S	R	K	283
GAG	AGT	GGA	AAG	AGT	GCT	GGG	ATT	CTT	ACT	CTT	CCC	ATC	ATG	AGC	AGA	AAT	TCC	CGG	AAA	993
T	I	G	K	W	R	V	B	Y	I	I	I	K	P	L	P	G	Y	S	C	303
ACA	ATA	GGC	AAA	GTG	AGA	GTT	GAC	TAT	ATA	ATT	ATT	AAG	CCA	TTA	CCA	GGA	TAC	AGT	TGT	1053
D	M	K	S	S	F	S	K	Y	W	K	P	R	I	P	L	D	V	G	H	323
GAC	ATG	AAA	TCT	TCA	TTT	TCC	AAG	TAT	TGG	AAG	CCA	AGA	ATA	CCA	TTG	GAT	GTT	GGC	CAT	1113
R	G	A	G	N	S	T	T	T	A	Q	L	A	K	V	Q	E	N	T	I	343
CGA	GGT	GCA	GGA	AAC	TCT	ACA	ACA	ACT	GCC	CAG	CTG	GCT	AAA	GTT	CAA	GAA	AAT	ACT	ATT	1173
A	S	L	R	N	A	A	S	H	G	A	A	F	V	E	F	D	V	H	L	363
GCT	TCT	TTA	AGA	AAT	GCT	GCT	AGT	CAT	GGT	GCA	GCC	TTT	GTA	GAA	TTT	GAC	GTA	CAC	CTT	1233
S	K	D	F	V	P	V	V	Y	H	D	L	T	C	C	L	T	M	K	K	383
TCA	AAG	GAC	TTT	GTG	CCC	GTG	GTA	TAT	CAT	GAT	CTT	ACC	TGT	TGT	TTG	ACT	ATG	AAA	AAG	1293
K	F	D	A	D	P	V	E	L	F	E	I	P	V	K	E	L	T	F	D	403
AAA	TTT	GAT	GCT	CCA	GTT	GAA	TTA	TTT	GAA	ATT	CCA	GTA	AAA	GAA	TTA	ACA	TTT	GAC	1353	
Q	L	Q	L	L	K	L	T	H	V	T	A	L	K	S	K	D	R	K	E	423
CAA	CTC	CAG	TTG	TTA	AAG	CTC	ACT	CAT	GTG	ACT	GCA	CTG	AAA	TCT	AAG	GAT	CGG	AAA	GAA	1413
S	V	V	Q	E	E	N	S	F	S	E	N	Q	P	F	P	S	L	K	M	443
TCT	GTG	GTT	CAG	GAG	GAA	AAT	TCC	TTT	TCA	GAA	AAT	CAG	CCA	TTT	CCT	TCT	TTT	AAG	ATG	1473
V	L	E	S	L	P	E	D	V	G	F	N	I	E	I	K	W	I	C	Q	463
GTT	TTA	GAG	TCT	TTG	CCA	GAA	GAT	GTA	GGG	TTT	AAC	ATT	GAA	ATA	AAA	TGG	ATC	TGC	CAG	1533
Q	R	D	G	M	W	D	G	N	L	S	T	Y	F	D	M	N	L	F	L	483
CAA	AGG	GAT	GGG	ATG	TGG	GAT	GGT	AAC	TTA	TCA	ACA	TAT	TTT	GAC	ATG	AAT	CTG	TTT	TTG	1593
D	I	I	L	K	T	V	L	E	N	S	G	K	R	R	I	V	F	S	S	503
GAT	ATA	ATT	TTA	AAA	ACT	GTT	TTA	GAA	AAT	TCT	GGG	AAG	AGG	AGA	ATA	GTG	TTT	TCT	TCA	1653
F	D	A	D	I	C	T	M	V	R	Q	K	Q	N	K	Y	P	I	L	F	523
TTT	GAT	GCA	GAT	ATT	TGC	ACA	ATG	GTT	CGG	CAA	AAG	CAG	AAC	AAA	TAT	CCG	ATA	CTA	TTT	1713
L	T	Q	G	K	S	E	I	Y	P	E	L	M	D	L	R	S	R	T	T	543
TTA	ACT	CAA	GGA	AAA	TCT	GAG	ATT	TAT	CCT	GAA	CTC	ATG	GAC	CTC	AGA	TCT	CGG	ACA	ACC	1773
P	I	A	M	S	F	A	Q	F	E	N	L	L	G	I	N	V	H	T	E	563
CCC	ATT	GCA	ATG	AGC	TTT	GCA	CAG	TTT	GAA	AAT	CTA	CTG	GGG	ATA	ATT	GTA	CAT	ACT	GAA	1833

FIGURE 4B

D	L	L	R	N	P	S	Y	I	Q	E	A	K	A	K	G	L	V	I	F	583
GAC	TTG	CTC	AGA	AAC	CCA	TCC	TAT	ATT	CAA	GAG	GCA	AAA	GCT	AAG	GGA	CTA	GTC	ATA	TTC	1893
C	W	G	D	D	T	N	D	P	E	N	R	R	K	L	K	E	L	G	V	603
TGC	TGG	GGT	GAT	GAT	ACC	AAT	GAT	CCT	GAA	AAC	AGA	AGG	AAA	TTG	AAG	GAA	CTT	GGA	GTT	1953
N	G	L	I	Y	D	R	I	Y	D	W	M	P	E	Q	P	N	I	F	Q	623
AAT	GGT	CTA	ATT	TAT	GAT	AGG	ATA	TAT	GAT	TGG	ATG	CCT	GAA	CAA	CCA	AAT	ATA	TTC	CAA	2013
V	E	Q	L	E	R	L	K	Q	E	L	P	E	L	K	S	C	L	C	P	643
GTG	GAG	CAA	TTG	GAA	CGC	CTG	AAG	CAG	GAA	TTG	CCA	GAG	CTT	AAG	AGC	TGT	TTG	TGT	CCC	2073
T	V	S	R	F	V	P	S	S	L	C	G	E	S	D	I	H	V	D	A	663
ACT	GTT	AGC	CGC	TTT	GTT	CCC	TCA	TCT	TTG	TGT	GGG	GAG	TCT	GAT	ATC	CAT	GTG	GAT	GCC	2133
N	G	I	D	N	V	E	N	A	*											673
AAC	GGC	ATT	GAT	AAC	GTG	GAG	AAT	GCT	TAG											2163
TTTTTATTGCACAGAGGTATTTGGGGCGTGCACCGCTGTTCTGGTATTCACTTTCACTGAGCATTGTTGAT																				2242
CTATGCCTTTGGGCTTCTCAGTCAATGAAGCAATAATGAAGTATTAACTCTTCACTACAGTTGCAAGTATGC																				2321
TATTTAAATTACTGGCCAGGTATAATTGCCAGTCAGTCTTTATAGTGAGAAAATTATTGGTTAGTAATATAAATA																				2400
TTTTAACTAAATATATAATCTATAATGTTAACATATGTCATTAAGCAGTACACTTGAAATTAACTATATAAA																				2479
TAGCTCATATTACACTTACAGCTTTCATTGATCAGGTCTGAAATCTTAGCACTTAAGGAAAATGACTATGCATAA																				2558
TTATACCTGACCATGAAAAAAATAAGTACCTCAATGCATGCATTGCACTGGTGATTCAACTGCACAAATCTTGTG																				2637
CCATCTGTATATAGGTATTTTACATGGGTTGACATGCACACAAACACCATTTCATTCACTGATGAACTTGAGGCTG																				2716
CTGCCATTTCCACTTAACCAAACCGCCTGAAGGTGAACCTCGAAACTTGTTCATAAAATCTTCAAAAGTTGTTT																				2795
ACATCAATGTTAAAATTCAAAATGCTGCAGGGTAATTAAATGTATAAAATATTAGTAAGAAAAGTATGTATTGCATA																				2874
CTTAGTAGAATAGATCACAACATACAATTCAATTCACTGCTTGTGGTGAGGTGAGATGCAAGGACTGGACGTATTGTTGCCTAAAAAAA																				2953
TGTTAGGTCTTGCATCTGTGGTGCTAGGTGAGTATGAGAAGATGTCAGGACTGGACGTATTGTTGCCTAAAAAAA																				3032
AAAGGCTGTTGTAGCGTTAAATATGCTTATTTGTGTCTCACTACCTATTACACACTGTTGCTTGTGGGT																				3111
TTGTTTTGTATGTGCGTGTATACAGTAGTTAAATTCCATGCAGAAAATAATGTCCTGAATTCTCAAAAAAAA																				3190
AAAAAAGGGCGGCCGC																				3206

FIGURE 4C

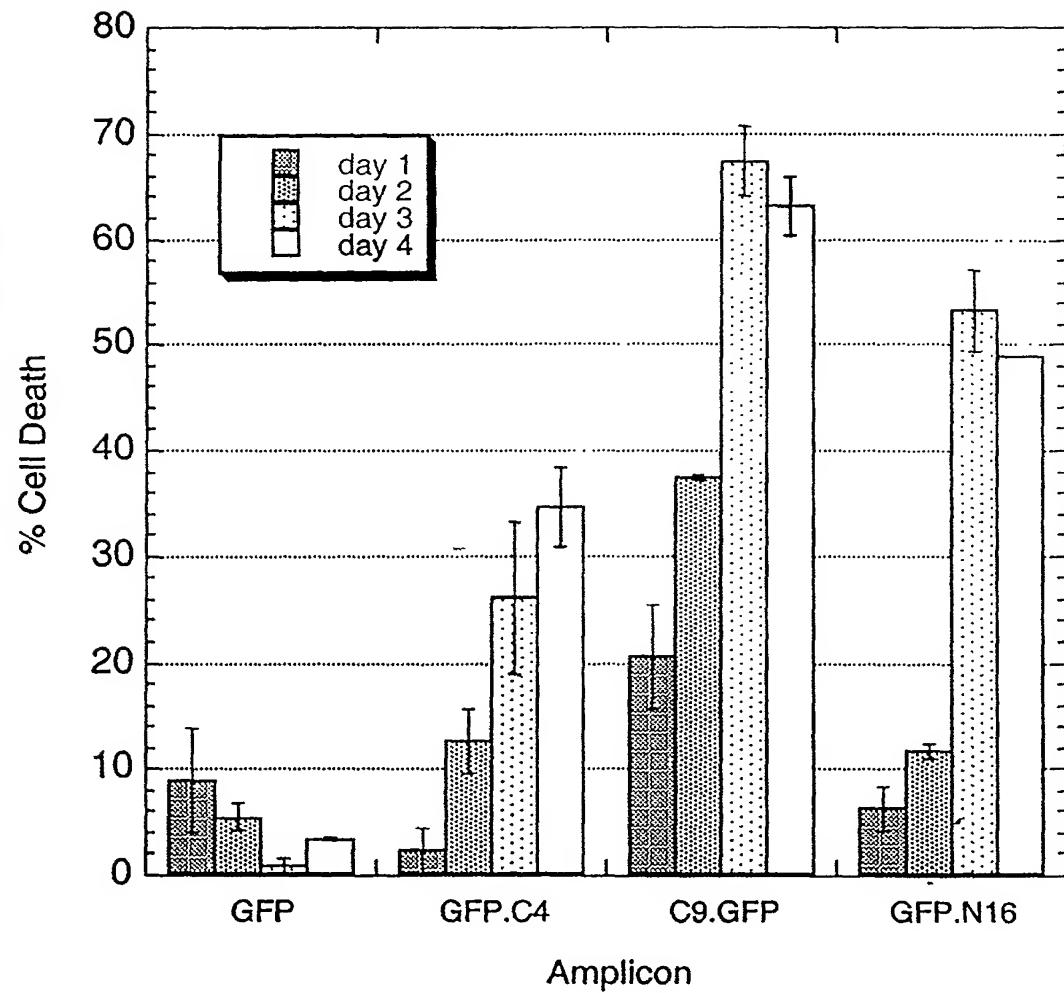


FIGURE 5